

APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	530	387.

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACGTGT
GTTGAAGGGTGTTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG
TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAA CTTCTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCCTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTCTCTGGCTTTGTGCTCTGCCAAACCCCTTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACTCTCTTTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTTTCCA
TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTACGAGTTGTACATTGCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC
AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGGT
CTGATCCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTTCTAACCACAAAGAA
GTTGCGAAGGCTGTATCTGTCCCAATCAACTAAGTGAAATACCACTTAATCTTCCCAAAT
CATTAGCAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAA
GGAATGAATGCTTTACACGTTTTTGGAATGAGTGCAAACCCCTCTTGATAATAATGGGATAGA
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGCAGAAGCAAACTGACCT
CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCCTAGGAAACAA
CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT
TGGAAAACAATAAACTAAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGAGGAGTAAATGACTTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG
AAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTTTCACTTGGGAACCTTT
GGAATGTAATAATTAGTAATTTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT
TGGAATACTTGAACCTTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT
GATACATAAGGGGTGAGAGAAACAAGCATCTATTGCAGTTTTCTTTTTTGCGTACAAATGAT
CTTACATAAATCTCATGCTTGACCATTCTTTCTTCATAACAAAAAAGTAAGATATTTCGGTA
TTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT
TAGCAAAATTTGTGCTCTTTTCAATTTGCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCAATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTTAAT
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT
CTTTATGTTTAAACTAATTTCTTAAAATAAAGCCTTCAGTAAATGTTTATTACCAACTTGA
TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTTAATTATT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACTCGCATTTT
AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATTGTTAGGCTATATAACATTGCCAC
TTCAACTCTAAGGAATATTTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAAGAGCCTGGA
CACTAACAAATTCTACACCAAATTGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTTCTTTATGTATTTCTTATTGGCATTCACATATGTAAATCAGAAA
ACAGGGAAATTTTCATTAAAAATATTGGTTTGAAAT

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
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FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR
 SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
 TSLYGLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
 KDTFKGMNALHVLEMSANPLDNNGIEPGAPEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
 YNKISTVELEDFKRYKELQRLGLGNKITDIENGLANIIPRVREIHLENNKLKKIPSGLPEL
 KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
 QLGNFQM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCCGSGCACCGCCCCCGGCCCTCCGCCCTCCGCACTCGCGCCTCC
CTCCCTCCGCGCGTCCGCGGCCCTCCTCCCTCCCTCCTCCCCAGCTGTCCCGTTTCGCGTCAATGCCGAGCCTCCC
GGCCCCGCGCGCCCCGCTGCTGCTCCTCGGGTGTGCTGCTCGGCTCCCGGCCGGCCCCGCGCGCCCCGAG
GCCCCCGTGTGCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTCGGGGAGCGGCAGGCTGCACCTTCGGCGG
GAAGGTCTATGCCTTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTTCGGGGTGATGCGCTGCGTGCTGTG
CGCTGCGAGGCGCCTCAGTGGGGTGCCTGTACAGGGGCCCTGGCAGGGTCACTGCAAGAACATCAAACCAGA
GTGCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGCCAGACCTGCCCCAGGAGCGCAG
CAGTTCGGAGCGGCAGCCGAGCGGCCTGTCTTCGAGTATCCGCGGGACCCGGAGCATCGCAGTTATAGCGACCG
CGGGGAGCCAGGCGCTGAGGAGCGGGCCCCGTGGTGACGGCCACACGGACTTCGTGGCGCTGCTGACAGGGCCGAG
GTCGACGGCGGTGGCACGAGCCCCAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCTACAGGCGGCT
GGACCGCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTGTTGAGCACCTGCAGCCCCACCCA
AGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA
TGTGGCACTTGTGACACTCACTCACCCCTCAGGGGAGGTCTGGGGGCCCTCTCATCCGGCACCGGGCCCTGGCTGC
AGAGACCTTCAGTGCCATCCTGACTCTAGAAGGCCCCCCACAGCAGGGCGTAGGGGGCATCACCTGTCACTCT
CAGTGACACAGAGGACTCCTTGCATTTTTTGCTGCTCTTCCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC
CCAGGTTCCCTTGAGGCTCCAGATTCTACACAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCA
GGAACCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGGGGAGCTGCA
GATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGT
CCTGCAAAGTGTCTTTGTGGGGCTGATGCCCTGATCCAGTCCAGACGGGTGCTGCCGGCTCAGCCAGCCTCAC
GCTGCTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGACACT
GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCTGTGCCACATGGCTGGACTCCAGCCAGGAGGACACAC
GGCCGTGGGTATCTGCCCTGGGTGGGTGCCCGAGGGGCTCATATGCTGCTGCAGAATGAGCTCTTCTGAACGT
GGCCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCAGTGCTGCTGCCCTGCTTGTGGGCATAGCGCCCCG
CCATGACACGCTGCCCCGTGCCCTAGCAGGAGCCCTGGTGCTACCCCTGTGAAGAGCCAAGCAGCAGGGCACGC
CTGGCTTTCTTGATACCCACTGTACCTGCACTATGAAGTGTGCTGGCTGGGCTTGGTGGCTCAGAACAAAGG
CACTGTCACTGCCCACCTCCTTGGGCCCTCTGGAACGCCAGGGCCTCGCGGGCTGCTGAAGGGATTCTATGGCTC
AGAGGCCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAAGTGTGCGGCACCTGGCAAAAGGCATGGCCTCCCTGAT
GATCACCAACCAAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATAGCCAACCAATGTGAGGTTGGCGG
ACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCC
TGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGCAAACCTGGTGGTCTGGGCGGCCCGAGACCCCAACACATG
CTTCTTCGAGGGGCAGCAGCGCCCCCACGGGGCTCGCTGGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCAC
CTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCCGCCAGCTGCCACACCCGGTGCAGGCTCC
CGACCACTGCTGCCCTGTTTGCCCTGAGAAACAAGATGTGAGAGACTTGCCAGGGCTGCCAAGGAGCCGGGACCC
AGGAGAGGGCTGCTATTTTGATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCC
CTTTGGCTTAATTAAGTGTGCTGTCTGCACCTGCAAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCACTG
TCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAACAGTGTCCAGTGGGGTGGG
GGCCCCACCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGGGGTGGCGTTTTGCTGGGCAGTGGTTCCC
AGAGAGTCAAGCTGGCACCCCTCAGTGCCCCCTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGCAGG
GGTGCCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTGCATGCTGTTT
CCGCTGCACGGCCACCGCGGCCCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTA
GGGAGCAGCCAGAGGGCAAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT
GCATTCTCTGTGGGAAGCCAGTGCTTTGCTCCTCTGTCTGCTTACTCCCACCCCACTACCTCTGGGAA
CCACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCTGCCCCGCCACCC
TCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTTA
TCTTCACTCAGCACCAAGGGCCCCGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
TTTTGTATTATTAAACATTTCTTTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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APPROVED	O.G. FIG.	
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FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVIRGAAGCTFGGKGYALDE
 TWHPDLGQPFVGMRCVLCACEAPQWGRRTGPGRVSCNKKPECPTPACGQPRQLPGHCCQT
 CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAEEERARGDGHTDFVALLTGPRSQAVAR
 ARVSLLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL
 LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLSDTED
 SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPLNLTVQEMD
 WLVLGELQMALEWAGRPGRLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
 GSLIYQVQVVGTSSEVVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAAML
 LQNELFLNVGTKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS
 LDTHCHLHYEVLLAGLGSGEQGTVAHLLGPPGTPGPRLLKGFYGSQAQGVVKDLEPELLR
 HLAKGMAASLMITTKGSPRGELRGQVHIANQCEVGGLRLEAAGAEGVRALGAPDTASAAPPVV
 PGLPALAPAKPGGPGRPRDPNTCFFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP
 PPSCPHPVQAPDQCCPVCPEKQDVRDLPLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPFF
 GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVVNPNTDCCKQCPVGSAGHPQLGDPMQADG
 PRGCRFAGQWFPESQSWHPSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCGSGKESRCCS
 RCTAHRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
 390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
 576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
 905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

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FIGURE 5

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCGCCGTCCTGCG
TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGGCCATGCAGCCCCCGCGCGCCAGGCGCCCGGTGCGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG
CCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG
AGCCGGACCCGAGCACC CGCCCCCGCGCGAGCCTGGCTACAGCTGCACCTGCCCGCCGGGATCTCCGGCG
CCAACCTGCCAGCTTGTTCAGATCCTTGTGCCAGCAACCCTTGTACCATGGCAACTGCAGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACTTCCAGTC
TCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCTGCTACTCAGGAGCCTGACA
AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAAACAGGGCAGAAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTGCGCAAGATGCCACTGCCTCAGTATTGTC
TCTGGAAGGTACGCGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCTCAGGCTT
CAGGGGGACTGGTCTCTGAGGAGATGCTCGCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG
TGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTGACACCTGTGTGCCGGGGGAGAGTCAG
CAAATGACTTGGAGTGTTTCAAGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCTGTACCTGTG
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAAATACGATGCTTGGCAGAGGAAACCTTGCCAAAACAACGCGAGCT
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCTGGTTATACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCTTCAGAAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATCTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT
GCCAGAACAACGGCACCTTATGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCGCGAGCGTGGGCACAGCT
CCTGTGCCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
ACAAATGCCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCCTGGCAGAATACAAAGGAACAC
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTGAGTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA
ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCACATTGACATAAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGGAGCTGCCTGGACAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG
CAAACCTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC
TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTGCGCGA
TCAGCCGCATTGAATACCAGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACTGCCGCGAGCATCGACAGCG
AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCCCTGCAATGTATGATGTGA
GCCCCATCGCCTATGAAGATTACAGTCTCTGATGACAAACCCTTGGTCACACTGATTAATAAATAAAGATTGTAAAT
CTTTTTTTGGATTATTTTTTCAAAAAGATGAGATACTACACTCATTATAAATATTTTAAAGAAAATAAAAGCTTAA
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTTCAAGATAATTTAAGAACTAATTTCTGCAGCTTTTAGTTTG
GAAAAAATATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAAACTGT
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAAATTTCTGTGGTTGTTACA
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGGTGGCCTTTCTGAGTAGAGTTAGGAAAACCCAC
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAAGTCTGAAATGTTTCGTTTTGTGAAA
AGAACTAGTTAAATTTACTATTCTTAACCCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAAGTAAC
TTATTTCTGCACTGTTTTGTGAACTTTGTGGAACATTCTTTCGAGTTTGTTTTTGTCAATTTTCGTAACAGTCG
TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTTCTGATTGATTGTAATCTATATTT
TTCTTTAAAAAGTCAAGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTTCTTTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGTATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
AAGTCA

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FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLLGAGPRGSSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
 PEPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSSSDGYLCICN
 EGYEGPNCEQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV
 VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFG
 QCSLIDGRSVTPLQASGGLVLEEMLALGNNHFIGFVNDVTKSIVALRLTLVVKVSTCVPG
 ESHANDLECSGKGKCTTKPSEATFSCCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD
 GSNFTCVCLPGYTGELCQSKIDYICILDPICRNGATCISSLSGFTCCQCEGYFGSACEEKVDPC
 ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSTYKCLCDPG
 YHGLYCEEEYNECLSAAPCLNAATCRDLVNGYECVCLAEYKGTHCELYKDPCANVSCLNGATC
 DSDGLNGTCICAPGFTGEECDIDINECDSNPCHHGGSCLDQPNGYNCHCPHGWVGANCEIHL
 QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYFN
 CRSIDSEFSNAIASIRHARFGKKSPPAMYDVSPPIAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
 375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
 373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
 491-503, 529-541, 567-579, 605-617

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FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

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FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
 CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
 ATCACTTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
 CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
 AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
 AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
 GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
 TGGTTATACTGGAGAGCTTTGCCAACCGAACCTGAGATTGGAGCGAACGACCTACACCGAACT
 GAGATAGGGGAG

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BY	CLASS SUBCLASS
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FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTAACTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATA CGCCGCATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC
GGGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTCT
TCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCCTTGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGCAAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

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APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
 QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
 TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
 TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
 LLKKNNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
 DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEEKWQSPLEDKFPDEQLSSS
 CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

0044396-033001

APPROVED	U. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
 CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
 CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGACGGCCAC
 AACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
 CAATTTACGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT
 TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
 CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
 TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
 TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCGCTACCTGACGCTC
 ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
 CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
 TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
 GCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGTGTGTGCAACAGTGCTCGGAATGTTCC
 TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
 GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
 AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
 CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTTGATAGAGGAGTTGCTGAGTCGTG
 GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA
 GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCCTTGAGGACAAGTTCCCGGATGA
 GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT
 CAGGCCAGGAACCTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
 GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGA
 ACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCC AAAACCCAAGGACACC

09944396-083001

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
 QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSKALND
 TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
 TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
 LLKKNNGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
 DVSTYPVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
 CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP
 SVFLFPPKPKDT

0044396-083001

FIGURE 13

CGCCCAGCGACGTGCGGGCGGCCTGGCCCCGCGCCCTCCCGCGCCCGGCCTGCGTCCCGCGCC
 CTGCGCCACCGCCGCCGAGCCGAGCCCGCCGCGCGCCCCCGGCAGCGCCGGCCCCATGCCC
 GCCGGCCGCCGGGGCCCCGCCGCCAATCCGCGCGGGCGGCGCGCCGTTGCTGCCCCCTGCT
 GCTGCTGCTCTGCGTCCTCGGGGCGCCGCGAGCCGGATCAGGAGCCCACACAGCTGTGATCA
 GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGCACGGA
 GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCTCAACGGGCGCCGCCTGCCCCC
 TGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGT
 CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCCGTGACGGCAGCATCCTGGCTGGC
 TCCTGCCTCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA
 CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGGAGACCTTCCTCCACACCA
 ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC
 ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT
 CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCCGCTCCGATGTACTCACGCTGGATATCC
 TGGATGTGGTGACCACGGACCCCCCGCCCGACGTGCACGTGAGCCGCGTCGGGGGCCTGGAG
 GACCAGCTGAGCGTGCGCTGGGTGTGCGCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA
 ATACCAGATCCGCTACCGAGTGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA
 ACCAGACCTCCTGCCGCCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC
 TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACCC
 CACAGCCGCCTCCACTCCCCGAGTGAGCGCCCCGGGCCCCGGGCGGCGGGGCGTGCGAACCGC
 GGGGCGGAGAGCCGAGCTCGGGGCCGGTGCGGCGCGAGCTCAAGCAGTTCCTGGGCTGGCTC
 AAGAAGCACGCGTACTGCTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCCTGGAT
 GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA
 CGGCGAGAGGTCTGCCAGATTAAGCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGA
 CGCAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC
 CCTCAGCAGGAGCTGGGGTGGCCCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT
 GAGGCCACCTTTGGGTGCACCCCAGTGGGTGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
 CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC
 CCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTGAAAAAAAAAA
 AA

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
 AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
 GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTCATACCTTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
 GGCATTTCTTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
 CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
 TTTTCATAAACTTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAACAACATG
 TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
 ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
 CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
 AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA
 ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
 TCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
 CCAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
 AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT
 ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
 TGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
 ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
 AA
 AA

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
 LVLWDINKHGLEETAACKCKGLGAKVHTFVVDSCNREDIYSSAKKVKAIEIGDVSILVNNAGVV
 YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
 SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
 GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

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APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
 GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA
 CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
 GCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCTTGC
 TGCTCCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
 CCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG
 CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA
 GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
 CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
 CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG
 AGCAGGGACATTACGACGCCGTACCCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
 TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
 ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGG
 GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
 ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA
 CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
 TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATT
 GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAAC
 AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA
 GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
 GGGGTGCTCTCTTCCCTGGTCCTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG
 GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAA

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
 GEKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
 FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
 KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

T00000-9604-083001

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGCATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGACAGGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTIONCGAGACCAGGAACCTTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA
GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT
GGCAACTGCGTGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA
CCTTGACAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

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APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCGCCATGCTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCCTTCACTACGTTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAGGAATAAAACCACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTAG
AGCTTCTGCAGTGATTCCAGCAAGGACAAAGCCGCCTTTTTCCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGGCAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCAT
CTACTGTCATTAAACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA
AAGACCTTCTCCTTTACCCAAGAATGTGGTATTCTGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGTACATTACCATATGTCACCCACTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCCACGG
TCGGGGAGACGCACACCCTCAAGATCCTCAACAACACCCGAGAGGCCGCCGAGGCCAAGTC
TGCATCTTCACCATTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTGCGT
GGAGAACTGTGGCCTCACACGGCGCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCG
GGTTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTCACCGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCTGGAGGCGATGGAGAGGGGGACACCAACACATCGAGCGTCT
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGGCCGGTCCCACGCATGGATGGCCTGGAGGAGGCCACGG
CATGTCGGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAAAACAAAACAAAACAAAAAAGA
CATGGGAGAGATGGTGTTTTTCTCTCCACCACCTGGGGATACGATTGAGAAAGATGGCCACCT
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGGACCTC
CCAGCCTCCAGAAGTGTGAGAAATAAATGTGTTTTGTTTAAGCTAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 22

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
```

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLRLKTKPLMTEFSVKSTIIIS
RYAFTTVSCRMLNRASEDQDIEFQMQIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVFVLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVDRKLDHLHVEVTASNSKKFII LKTDVPVRPQKAGKDV TG
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTG TAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
 GGCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
 CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
 GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAGCTACTGAA
 TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT
 TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
 GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
 CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
 AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAA
 GGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
 CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
 AGCACCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
 CAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
 GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
 ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTCAATAACCTAAACAAA
 ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
 TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCA
 CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
 TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
 GCTGTGCTTGCTCATCATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
 ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
 GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTTGTTTCAAT
 GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

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APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
 QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQL
 YTDPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
 KSEVEEWSDMYTVTSQMLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
 YPLQGLTREGDALELTCEAIGKPQPMVMTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
 CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTILTIIITDSRAGEEGSIRAVDH
 AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
 KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
 430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
 411-417, 427-433, 428-432

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FIGURE 26

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804
```

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPDDTVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNIASLRLPRLLLLDLSHNSLLALEPGILDATANVEALRL
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFPFKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQ
GTRPSPTPVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRLTYRNLSPDKRLV
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFGPGLQSPHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

Figure 1

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCCGTACCCTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGACAGGAGGCCCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTTCCCATTAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTCACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCATAATTCCCCGG
GCAAGGGCGAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAAACTGTGATT
GTGTTATAAAAAGTGGCTCCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTC
CCCGTTCCTCACTTTTCCCTTTTCATTCCCACCCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

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APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 29

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC
TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCTTTGCTCTGGCCTGGT
CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC
GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG
ATCGAGGCCTCCAAGGGAAATATGGCAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGGCCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCGGCAAGTTCTACTGCTAC
GTGCCCCGGCCTCTACTTCTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCCGATCCCTGGACTCCGACTC
CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC
GAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGCGGCACCGCGGCTCCAGTCTTGAAATA
ATTAGGCAAATTTCTAAAGGTCTCAAAGGTAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTCAGTTGAG
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAAGGGAGGGGCCGGGGCAGG
AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTTCTTGAGGGATAGGTGGACC
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT
GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCTGGCATCGGCT
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGGCTAAGCATCACCGCTT
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCCGCTGTGTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATCACTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCC
ATAGCCCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC
CCCAAACCCCGCTGCCTCTCTTCCCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC
TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
GCTGCTTAAGCTCCCCAGCTCTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

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APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 31

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCGCGCGGATTGCGCCGGTCCTTCCCGCGG
 GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTTGCATTCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCCAAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATAACACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGGTGATAGGCC
 TCGTCTCTCGGGTAGAATCCTTTCGGAATCACTCCGCAGGAACGTTACTCAAGACTGGAT
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 TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTAGTAGAGACGGGGTTTACCAGTGTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTAAACTTATT
 CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED
 CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
 SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
 KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
 PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTTFQAP
 TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
 PENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

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APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

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APPROVED	U. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIGURE 34

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
```

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCI PKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

[illegible]